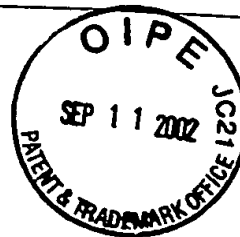


RECEIVED

SEP 18 2002

TECH CENTER 1600/2900

SEQUENCE LISTING



<110> Wake Forest University
Bowden, Donald W.
Dawson, Paul A.
Fossey, Sallyanne C.

<120> GLUT 10: A Novel Glucose Transporter in the Type 2 Diabetes Linked Region
of Chromosome 20Q12-13.1

<130> 9151-11.WO

<140> PCT/US 01/26184

<141> 2001-08-22

<150> US 09/652292

<151> 2000-08-31

<160> 28

<170> PatentIn version 3.1

<210> 1

<211> 4395

<212> M.A

<213> Homo sapiens

<220>

<221> CDS

<222> (250)..(1875)

<223>

COPY OF PAPERS
ORIGINALLY FILED

<400> 1

gaggggggtcc ttgccaggcc tggggcgcc gggggcggtc ctgggctccc ctccgtcccg 60

cctccaggcc tcggggcctg gctggccgac gtggcgttgg cggcgctgcg cgcgggaggg 120

cagggcagga gggacagagg cggggcggg ccgaaaagtt tgtccggcgg cagcggcggt 180

ggggactccg gcgggggatg cgcgcccggc cctcagcgc cccagcacg ccgcccagtc 240

ccgctcgcc atg ggc cac tcc cca cct gtc ctg cct ttg tgt gcc tct gtg 291

Met Gly His Ser Pro Val Leu Pro Leu Cys Ala Ser Val

1

5

10

tct ttg ctg ggt ggc ctg acc ttt ggt tat gaa ctg gca gtc ata tca 339

Ser Leu Leu Gly Gly Leu Thr Phe Gly Tyr Glu Leu Ala Val Ile Ser

15

20

25

30

ggt gcc ctg ctg cca ctg cag ctt gac ttt ggg cta agc tgc ttg gag 387

Gly Ala Leu Leu Pro Leu Gln Leu Asp Phe Gly Leu Ser Cys Leu Glu

35

40

45

cag gag ttc ctg gtg ggc agc ctg ctc ctg ggg gct ctc ctc gcc tcc 435

Gln Glu Phe Leu Val Gly Ser Leu Leu Leu Gly Ala Leu Leu Ala Ser

50

55

60

ctg gtt ggt ggc ttc ctc att gac tgc tat ggc agg aag caa gcc atc	483
Leu Val Gly Gly Phe Leu Ile Asp Cys Tyr Gly Arg Lys Gln Ala Ile	
65 70 75	
ctc ggg agc aac ttg gtg ctg ctg gca ggc agc ctg acc ctg ggc ctg	531
Leu Gly Ser Asn Leu Val Leu Leu Ala Gly Ser Leu Thr Leu Gly Leu	
80 85 90	
gct ggt tcc ctg ggc tgg ctg gtc ctg ggc cgc gct gtg gtt ggc ttc	579
Ala Gly Ser Leu Ala Trp Leu Val Leu Gly Arg Ala Val Val Gly Phe	
95 100 105 110	
gcc att tcc ctc tcc tcc atg gct tgc tgt atc tac gtg tca gag ctg	627
Ala Ile Ser Leu Ser Ser Met Ala Cys Cys Ile Tyr Val Ser Glu Leu	
115 120 125	
gtg ggg cca cgg cag cgg gga gtg ctg gtg tcc ctc tat gag gca ggc	675
Val Gly Pro Arg Gln Arg Gly Val Leu Val Ser Leu Tyr Glu Ala Gly	
130 135 140	
atc acc gtg ggc atc ctg ctc tcc tat gcc ctc aac tat gca ctg gct	723
Ile Thr Val Gly Ile Leu Leu Ser Tyr Ala Leu Asn Tyr Ala Leu Ala	
145 150 155	
ggt acc ccc tgg gga tgg agg cac atg ttc ggc tgg gcc act gca cct	771
Gly Thr Pro Trp Gly Trp Arg His Met Phe Gly Trp Ala Thr Ala Pro	
160 165 170	
gct gtc ctg caa tcc ctc agc ctc ctc ttc ctc cct gct ggt aca gat	819
Ala Val Leu Gln Ser Leu Ser Leu Leu Phe Leu Pro Ala Gly Thr Asp	
175 180 185 190	
gag act gca aca cac aag gac ctc atc cca ctc cag gga ggt gag gcc	867
Glu Thr Ala Thr His Lys Asp Leu Ile Pro Leu Gln Gly Gly Glu Ala	
195 200 205	
ccc aag ctg ggc ccg ggg agg cca cgg tac tcc ttt ctg gac ctc ttc	915
Pro Lys Leu Gly Pro Gly Arg Pro Arg Tyr Ser Phe Leu Asp Leu Phe	
210 215 220	
agg gca cgc gat aac atg cga ggc cgg acc aca gtg ggc ctg ggg ctg	963
Arg Ala Arg Asp Asn Met Arg Gly Arg Thr Thr Val Gly Leu Gly Leu	
225 230 235	
gtg ctc ttc cag caa cta aca ggg cag ccc aac gtg ctg tgc tat gcc	1011
Val Leu Phe Gln Gln Leu Thr Gly Gln Pro Asn Val Leu Cys Tyr Ala	
240 245 250	
tcc acc atc ttc agc tcc gtt ggt ttc cat ggg gga tcc tca gcc gtg	1059
Ser Thr Ile Phe Ser Ser Val Gly Phe His Gly Gly Ser Ser Ala Val	
255 260 265 270	
ctg gcc tct gtg ggg ctt ggc gca gtg aag gtg gca gct acc ctg acc	1107
Leu Ala Ser Val Gly Leu Gly Ala Val Lys Val Ala Ala Thr Leu Thr	
275 280 285	

Sub
C1
cons

gac atg ggg ctg gtg gac cgt gca ggc cgc agg gct ctg ttg cta gct 1155
Ala Met Gly Leu Val Asp Arg Ala Gly Arg Arg Ala Leu Leu Leu Ala
290 295 300

ggc tgc gcc ctc atg gcc ctg tcc gtc agt ggc ata ggc ctc gtc agc 1203
Gly Cys Ala Leu Met Ala Leu Ser Val Ser Gly Ile Gly Leu Val Ser
305 310 315

ttt gcc gtg ccc atg gac tca ggc cca agc tgt ctg gct gtg ccc aat 1251
Phe Ala Val Pro Met Asp Ser Gly Pro Ser Cys Leu Ala Val Pro Asn
320 325 330

gcc acc ggg cag aca ggc ctc cct gga gac tct ggc ctg ctg cag gac 1299
Ala Thr Gly Gln Thr Gly Leu Pro Gly Asp Ser Gly Leu Leu Gln Asp
335 340 345 350

tcc tct cta cct ccc att cca agg acc aat gag gac caa agg gag cca 1347
Ser Ser Leu Pro Pro Ile Pro Arg Thr Asn Glu Asp Gln Arg Glu Pro
355 360 365

atc ttg tcc act gct aag aaa acc aag ccc cat ccc aga tct gga gac 1395
Ile Leu Ser Thr Ala Lys Lys Thr Lys Pro His Pro Arg Ser Gly Asp
370 375 380

ccc tca gcc cct cct cgg ctg gcc ctg agc tct gcc ctc cct ggg ccc 1443
Pro Ser Ala Pro Pro Arg Leu Ala Leu Ser Ser Ala Leu Pro Gly Pro
385 390 395

cct ctg ccc gct cgg ggg cat gca ctg ctg cgc tgg acc gca ctg ctg 1491
Pro Leu Pro Ala Arg Gly His Ala Leu Leu Arg Trp Thr Ala Leu Leu
400 405 410

tgc ctg atg gtc ttt gtc agt gcc ttc tcc ttt ggg ttt ggg cca gtg 1539
Cys Leu Met Val Phe Val Ser Ala Phe Ser Phe Gly Phe Gly Pro Val
415 420 425 430

acc tgg ctt gtc ctc agc gag atc tac cct gtg gag ata cga gga aga 1587
Thr Trp Leu Val Leu Ser Glu Ile Tyr Pro Val Glu Ile Arg Gly Arg
435 440 445

gcc ttc gcc ttc tgc aac agc ttc aac tgg ggc gcc aac ctc ttc atc 1635
Ala Phe Ala Phe Cys Asn Ser Phe Asn Trp Ala Ala Asn Leu Phe Ile
450 455 460

agc ctc tcc ttc ctc gat ctc att ggc acc atc ggc ttg tcc tgg acc 1683
Ser Leu Ser Phe Leu Asp Leu Ile Gly Thr Ile Gly Leu Ser Trp Thr
465 470 475

ttc ctg ctc tac gga ctg acc gct gtc ctc ggc ctg ggc ttc atc tat 1731
Phe Leu Leu Tyr Gly Leu Thr Ala Val Leu Gly Leu Gly Phe Ile Tyr
480 485 490

tta ttt gtt cct gaa aca aaa ggc cag tgc ttg gca gag ata gac cag 1779
Leu Phe Val Pro Glu Thr Lys Gly Gln Ser Leu Ala Glu Ile Asp Gln
495 500 505 510

cag ttc cag aag aga cgg ttc acc ctg agc ttt ggc cac agg cag aac 1827

Gln Phe Gln Lys Arg Arg Phe Thr Leu Ser Phe Gly His Arg Gln Asn
515 520 525

tcc act ggc atc ccg tac agc cgc atc gag atc tct gcg gcc tcc tga 1875
Ser Thr Gly Ile Pro Tyr Ser Arg Ile Glu Ile Ser Ala Ala Ser
530 535 540

ggaatccgtc cgcttggaa tctggaactg tggctttggc agaccatctc cagcatcctg 1935

cttcctaggc ccagagcac aagttccagc tggcttttg ggagtggccc ctgccccaa 1995

aggtggtttg cttttgctgg ggtaaaaagg atgaaagttt gagaatgcc aattcttcat 2055

tttgggtttc aggcctgaa ggttcttgag gatctagttt catgcctcgg tttccccatt 2115

gacttggaaca tttttgcagt ttttataaga agaataattt atgaagtctt tgttgcccca 2175

tggatTTTT tcaaagaatc tcaggggtac caatccgggc aggaggtttt tcccgatata 2235

accctaaat ccaaataagg atatcatctt ttctaattct ttttttcaac tggctgggac 2295

attttcgga gggggaagtc tcttttttta ctcttatcat tttttttttt tgaggtggag 2355

tctcattctg ttgccaggc tggcctgac ttggctcact gcaacctcca cttcctgggt 2415

tcaagcgatt ctctgcctc agcctcctaa gtagctggga ttacaggcgc gtgccaccac 2475

accagctaa tttattttta gcagagatgg ggtttcactg tgttggccag gctggtcgtg 2535

aactcctgag ctcaagtgat ccaccacct cagcctccca gagtgcagg attacaggcc 2595

ttttgactct tttatctgag ttttattgac ccctctaatt ctcttaccga gaatatttat 2655

ccttcaccag caactctgac tctttgacgg gagcctcag ttctagtcct tggctcgtg 2715

gtgtcattgc tgtaggaatg accacgggccc tcagtttccc catttgata atgggaagcc 2775

tgtaccaggt cattcttaag atttctcctg actccagtga gctggaattc taaatgctgg 2835

tctaggagct gtctccagga tgggtcagga tggctttgag gaaaggagat gggtttgag 2895

gccaacaaac ctgcttgta atattgcctt tgctcttgg cagcccttga acttgagtaa 2955

ataacaactc cctgaacctc agtttcctca tctgcagaat ggggataatt atgtcccagg 3015

ggtatattta gacctgttt cttttcagga ggggtcccag ctggtccagg gcctgggaaa 3075

tttctactta tctcattac ccaggtccct cttttggacc ctgtaaaggg tcagggtgaa 3135

tcagatgggg gactgagcaa gtagctatga ctgcagatca tgtaaggag ggactgacaa 3195

gaagctccca gatgctgggg agaataaga gctaaaatag atcctaggtg ctggatgctt 3255

tgatcatcat gcgtgcacat atgggtgctg gcagagcccc caaggactct ggcctctcga 3315

gttctcctat cttctccatt ctatagctt cccttgatc cagtgatgtg ctggagctgg 3375

ctttgcgaag cttgtgagag ctggttgcta cattttcagg attttttacaa gttggtaaac 3435
 acagccatta taaaaaatta aatgatttaa atttataatt aagtaaatta cattaaaaca 3495
 aaaaaattat actcaaaatt cactacttaa ttttactacc tgttactatt atctgtgctt 3555
 ttgaggctat ttctacatag taactcttat ggagacctag gggagacacc gcgcattctt 3615
 tcctgattcc ccactcaatg acatcatggt agtctttggt tgcttaactg gctgtgggga 3675
 gtgtttttgt atcacaaga ttagagagga ctacacatca gggcttgatt tattgtttgt 3735
 tgattttcta gacttcagaa catgctggat aaaatgtcag taatgcaaata taaacttta 3795
 agtatgtctt gttttagacc aatacatggt gtatagcacc aaaaaatgga gggattattc 3855
 ttccagtagt tgaacactgt catccgtttc agctgacagc tgctcaaatac atttaagaag 3915
 gagttctgac attcattttc attgtttttac ttttgtcttc ctactagtgt taaacaaaaa 3975
 tttcaaccag cattcatgcc gaacctatac ccattcttca gtgcctagct gtacagttat 4035
 cagggatttt tattegtagt ctaattttgt caaatcatgg ccaaatacgca gtgatagttg 4095
 actttggata caagggtttg caaaaaaaa aatattaaca aaatattctg taagaatcaa 4155
 ttggctatat ggaatttagg ataaagaata ttacaataa agaataatta caataaagag 4215
 tttattatta tttgtaagtt gtgtgcaaca aacataacct ttatctctgt aaaatttata 4275
 cacacaaaaa ttaacaaaag attctgtaag aattaattgg ctatatggaa tttaggatag 4335
 aatattttaca ataaagagta tttacaataa agagttttgt attattttgta aaaaaaaaaa 4395

<210> 2
 <211> 541
 <212> PRT
 <213> Homo sapiens

<400> 2

Met Gly His Ser Pro Pro Val Leu Pro Leu Cys Ala Ser Val Ser Leu
1 5 10 15

Leu Gly Gly Leu Thr Phe Gly Tyr Glu Leu Ala Val Ile Ser Gly Ala
20 25 30

Leu Leu Pro Leu Gln Leu Asp Phe Gly Leu Ser Cys Leu Glu Gln Glu
35 40 45

Phe Leu Val Gly Ser Leu Leu Leu Gly Ala Leu Leu Ala Ser Leu Val
50 55 60

Gly Gly Phe Leu Ile Asp Cys Tyr Gly Arg Lys Gln Ala Ile Leu Gly
65 70 75 80

Ser Asn Leu Val Leu Leu Ala Gly Ser Leu Thr Leu Gly Leu Ala Gly
85 90 95

Ser Leu Ala Trp Leu Val Leu Gly Arg Ala Val Val Gly Phe Ala Ile
100 105 110

Ser Leu Ser Ser Met Ala Cys Cys Ile Tyr Val Ser Glu Leu Val Gly
115 120 125

Pro Arg Gln Arg Gly Val Leu Val Ser Leu Tyr Glu Ala Gly Ile Thr
130 135 140

Val Gly Ile Leu Leu Ser Tyr Ala Leu Asn Tyr Ala Leu Ala Gly Thr
145 150 155 160

Pro Trp Gly Trp Arg His Met Phe Gly Trp Ala Thr Ala Pro Ala Val
165 170 175

Leu Gln Ser Leu Ser Leu Leu Phe Leu Pro Ala Gly Thr Asp Glu Thr
180 185 190

Ala Thr His Lys Asp Leu Ile Pro Leu Gln Gly Gly Glu Ala Pro Lys
195 200 205

Leu Gly Pro Gly Arg Pro Arg Tyr Ser Phe Leu Asp Leu Phe Arg Ala
210 215 220

Arg Asp Asn Met Arg Gly Arg Thr Thr Val Gly Leu Gly Leu Val Leu
225 230 235 240

Phe Gln Gln Leu Thr Gly Gln Pro Asn Val Leu Cys Tyr Ala Ser Thr
245 250 255

Ile Phe Ser Ser Val Gly Phe His Gly Gly Ser Ser Ala Val Leu Ala
260 265 270

Ser Val Gly Leu Gly Ala Val Lys Val Ala Ala Thr Leu Thr Ala Met
275 280 285

Gly Leu Val Asp Arg Ala Gly Arg Arg Ala Leu Leu Leu Ala Gly Cys
290 295 300

Ala Leu Met Ala Leu Ser Val Ser Gly Ile Gly Leu Val Ser Phe Ala
305 310 315 320

Val Pro Met Asp Ser Gly Pro Ser Cys Leu Ala Val Pro Asn Ala Thr
325 330 335

Gly Gln Thr Gly Leu Pro Gly Asp Ser Gly Leu Leu Gln Asp Ser Ser
340 345 350

Leu Pro Pro Ile Pro Arg Thr Asn Glu Asp Gln Arg Glu Pro Ile Leu
355 360 365

Ser Thr Ala Lys Lys Thr Lys Pro His Pro Arg Ser Gly Asp Pro Ser
370 375 380

Ala Pro Pro Arg Leu Ala Leu Ser Ser Ala Leu Pro Gly Pro Pro Leu
385 390 395 400

Pro Ala Arg Gly His Ala Leu Leu Arg Trp Thr Ala Leu Leu Cys Leu
405 410 415

Met Val Phe Val Ser Ala Phe Ser Phe Gly Phe Gly Pro Val Thr Trp
420 425 430

Leu Val Leu Ser Glu Ile Tyr Pro Val Glu Ile Arg Gly Arg Ala Phe
435 440 445

Ala Phe Cys Asn Ser Phe Asn Trp Ala Ala Asn Leu Phe Ile Ser Leu
450 455 460

Ser Phe Leu Asp Leu Ile Gly Thr Ile Gly Leu Ser Trp Thr Phe Leu
465 470 475 480

Leu Tyr Gly Leu Thr Ala Val Leu Gly Leu Gly Phe Ile Tyr Leu Phe
485 490 495

Val Pro Glu Thr Lys Gly Gln Ser Leu Ala Glu Ile Asp Gln Gln Phe
500 505 510

Gln Lys Arg Arg Phe Thr Leu Ser Phe Gly His Arg Gln Asn Ser Thr

515

520

525

Gly Ile Pro Tyr Ser Arg Ile Glu Ile Ser Ala Ala Ser
 530 535 540

<210> 3
 <211> 20
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Synthetic oligonucleotide

<400> 3
 ggcacctctt ccctgcaaag 20

<210> 4
 <211> 20
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Synthetic oligonucleotide

<400> 4
 ccctcccgcg cgcagcgccg 20

<210> 5
 <211> 18
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Synthetic oligonucleotide

<400> 5
 cgtcccgctt ccaggcct 18

<210> 6
 <211> 17
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Synthetic oligonucleotide

<400> 6
 ccatggcgag cgggact 17

<210> 7
 <211> 18

<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 7
cgtcccgccct ccaggcct

18

<210> 8
<211> 19
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 8
ggcgggtgtct acacctctgg

19

<210> 9
<211> 21
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 9
tgacagatgg aggggaaggtt g

21

<210> 10
<211> 19
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 10
aggagcaggc tgcccacca

19

<210> 11
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 11
ctggcagtca tatcaggtgc

20

<210> 12
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 12
aatggcgaag ccaaccacag 20

<210> 13
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 13
ggagcaactt ggtgctgctg 20

<210> 14
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 14
agtggcccag ccgaacatgt 20

<210> 15
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 15
ctcaactatg cactggctgg 20

<210> 16
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 16
cggagctgaa gatggtggag 20

<210> 17
<211> 21
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 17
ctcttcagc aactaacagg g 21

<210> 18
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 18
agcttgggcc tgagtcacg 20

<210> 19
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 19
agtggcatag gcctcgtag 20

<210> 20
<211> 21
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 20
agaagtctcc agagtcacct g 21

<210> 21
<211> 21
<212> DNA
<213> Artificial sequence

~~<220>
 <223> Synthetic oligonucleotide

 <400> 21
 ggctgcatgt ttgacctgat g 21

 <210> 22
 <211> 21
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 22
 gcttttagagt agggagcttg g 21

 <210> 23
 <211> 21
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 23
 tgacctagaa cctaccagtt g 21

 <210> 24
 <211> 20
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 24
 tcctgaagct gtgtgcttgg 20

 <210> 25
 <211> 19
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Synthetic oligonucleotide

 <400> 25
 gggaaccca gtggaaggt 19

 <210> 26
 <211> 20~~

Sub
 C1
 cont

<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 26
caggcagacg gattcctcag

20

<210> 27
<211> 19
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 27
aactccactg gcatcccg

19

<210> 28
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic oligonucleotide

<400> 28
catgaaacta gatcctcaag

20

Sub
C1
cont
Q2
cont